

1/14

Cancelled and replaced
with substituted figures
1-6, submitted Dec. 19, 2002

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10/2/03

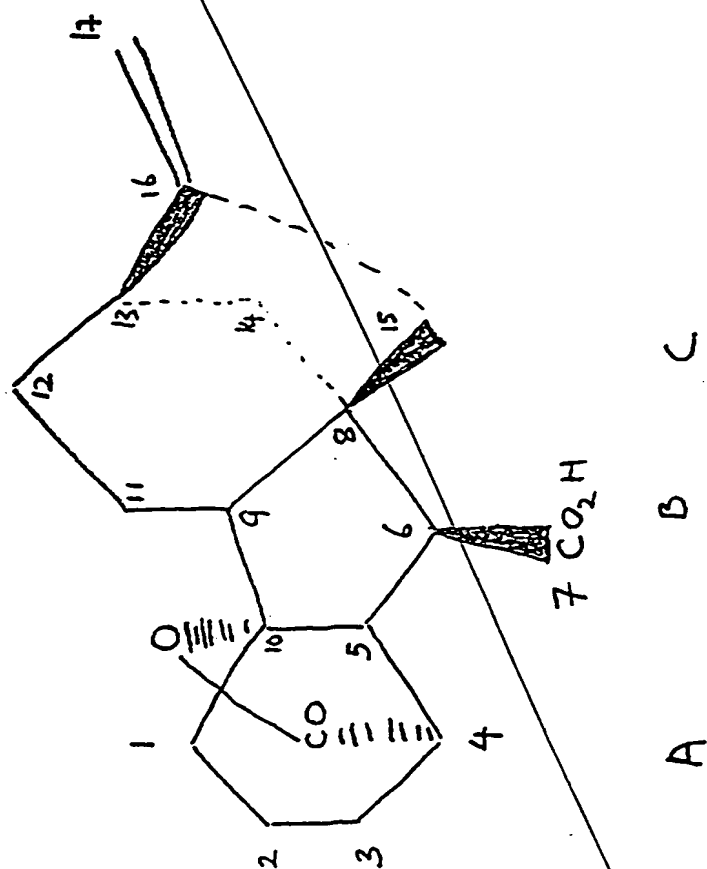


Fig. 1

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T05270-07500

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Fig. 2 b

GAI
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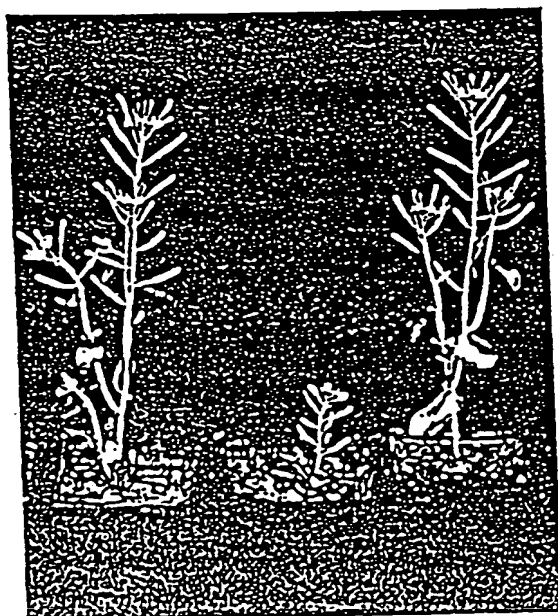
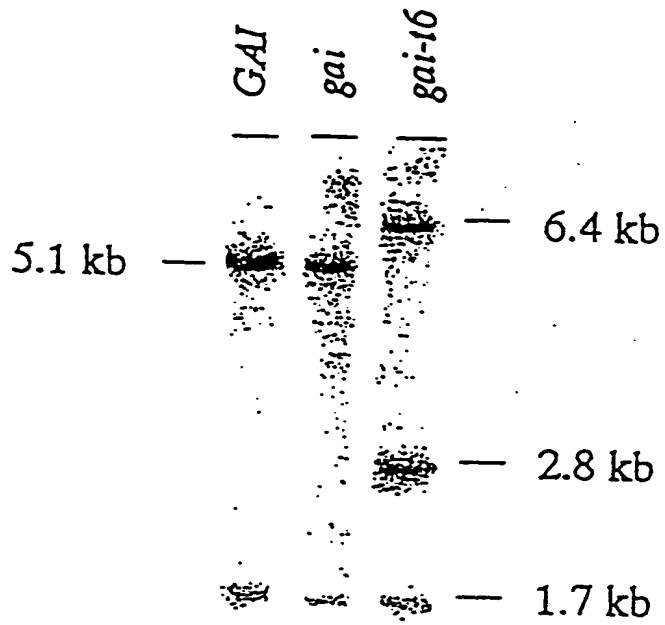
 = 18 kb
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Fig. 2 a

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Fig. 2c

T03270"CT9TT660

TAATAATCAT	TTTTTTTCTT	ATAACCTTCC	TCTCTATTTT	TACAATTTAT	TTTGTTATTA	60
GAAGTGGTAG	TGGAGTGAAA	AAACAAATCC	TAAGCAGTCC	TAACCGATCC	CCGAAGCTAA	120
AGATTCTTCA	CCTTCCCAAA	TAAAGCAAAA	CCTAGATCCG	ACATTGAAGG	AAAAACCTTT	180
TAGATCCATC	TCTGAAAAAA	AACCAACCAT	GAAGAGAGAT	CATCATCATC	ATCATCAAGA	240
TAAGAAGACT	ATGATGATGA	ATGAAGAAGA	CGACGGTAAC	GGCATGGATG	AGCTTCTAGC	300
TGTTCTTGCT	TACAAGGTTA	GGTCATCGGA	AATGGCTGAT	GTGCTCAGA	AACTCGAGCA	360
GCTTGAAGTT	ATGATGTCTA	ATGTTCAAGA	AGACGATCTT	TCTCAACTCG	CTACTGAGAC	420
TGTTCACTAT	AATCCGGCGG	AGCTTTACAC	GTGGCTTGAT	TCTATGCTCA	CCGACCTTAA	480
TCCTCCGTCG	TCTAACGCCG	AGTACGATCT	TAAAGCTATT	CCCGGTGACG	CGATTCTCAA	540
TCAGTTCCGT	ATCGATTCGG	CTTCTTCGTC	TAACCAAGGC	GGCGGAGGAG	ATACGTATAC	600
TACAAACAAG	CGGTTGAAAT	GCTCAAACGG	CGTCGTGGAA	ACCACCACAG	CGACGGCTGA	660
GTCAACTCGG	CATGTTGTCC	TGGTTGACTC	GCAGGAGAAC	GGTGTGCGTC	TCGTTACAGC	720
GCTTTTGGCT	TGCGCTGAAG	CTGTTTCAGAA	GGAGAATCTG	ACTGTGGCGG	AAGCTCTGGT	780
GAAGCAAATC	GGATTCTTAG	CTGTTTCTCA	AATCGGAGCT	ATGAGAAAAG	TCGCTACTTA	840
CTTCGCCGAA	GCTCTCGCGC	GGCGGATTTA	CCGTCTCTCT	CCGTCGCAGA	GTCCAATCGA	900
CCACTCTCTC	TCCGATACTC	TTCAGATGCA	CTTCTACGAG	ACTTGTCTTT	ATCTCAAGTT	960
CGCTCACTTC	ACGGCGAATC	AAGCGATTCT	CGAAGCTTTT	CAAGGGAAGA	AAAGAGTTCA	1020
TGTCATTGAT	TTCTCTATGA	GTCAAGGTCT	TCAATGGCCG	GCGCTTATGC	AGGCTCTTGC	1080
GCTTCGACCT	GGTGGTCCTC	CTGTTTTCCG	GTTAACCGBA	ATTGGTCCAC	CGGCACCGGA	1140
TAATTTTCGAT	TATCTTCATG	AAGTTGGGTG	TAAGCTGGCT	CATTTAGCTG	AGGCGATTCA	1200
CGTTGAGTTT	GAGTACAGAG	GATTTGTGGC	TAACACTTTA	GCTGATCTTG	ATGCTTCGAT	1260
GCTTGAGCTT	AGACCAAGTG	AGATTGAATC	TGTTGCGGTT	AACTCTGTTT	TCGAGCTTCA	1320
CAAGCTCTTG	GGACGACCTG	GTGCGATCGA	TAAGGTTCTT	GGTGTGGTGA	ATCAGATTAA	1380
ACCGGAGATT	TTCACTGTGG	TTGAGCAGGA	ATCGAACCAT	AATAGTCCGA	TTTTCTTAGA	1440
TCGGTTTACT	GAGTCGTTGC	ATTATTACTC	GACGTTGTTT	GACTCGTTGG	AAGGTGTACC	1500
GAGTGGTCAA	GACAAGGTCA	TGTCGGAGGT	TTACTTGGGT	AAACAGATCT	GCAACGTTGT	1560
GGCTTGTGAT	GGACCTGACC	GAGTTGAGCG	TCATGAAACG	TTGAGTCAGT	GGAGGAACCG	1620
GTTCCGGTCT	GCTGGGTTTG	CGGCTGCACA	TATTGGTTTCG	AATGCGTTTA	AGCAAGCGAG	1680
TATGCTTTTG	GCTCTGTTCA	ACGGCGGTGA	GGGTTATCGG	GTGGAGGAGA	GTGACGGCTG	1740
TCTCATGTTG	GGTTGGCACA	CACGACCGCT	CATAGCCACC	TCGGCTTGGA	AACTCTCCAC	1800
CAATTAGATG	GTGGCTCAAT	GAATTGATCT	GTTGAACCGG	TTATGATGAT	AGATTTCCGA	1860
CCGAAGCCAA	ACTAAATCCT	ACTGTTTTTC	CCTTTGTAC	TTGTTAAGAT	CTTATCTTTC	1920
ATTATATTAG	GTAATTGAAA	AATTTCTAAA	TTACTCACAC	TGGC		1964

Fig. 3

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MetLysArgAspHisHisHisHisHisGlnAspLysLysThrMetMetMetAsnGluGlu 20
 AspAspGlyAsnGlyMetAspGluLeuLeuAlaValLeuGlyTyrLysValArgSerSer 40
GluMetAlaAspValAlaGlnLysLeuGluGlnLeuGluValMetMetSerAsnValGln 60
 GluAspAspLeuSerGlnLeuAlaThrGluThrValHisTyrAsnProAlaGluLeuTyr 80
 ThrTrpLeuAspSerMetLeuThrAspLeuAsnProProSerSerAsnAlaGluTyrAsp 100
 LeuLysAlaIleProGlyAspAlaIleLeuAsnGlnPheAlaIleAspSerAlaSerSer 120
 SerAsnGlnGlyGlyGlyGlyAspThrTyrThrThrAsnLysArgLeuLysCysSerAsn 140
 GlyValValGluThrThrThrAlaThrAlaGluSerThrArgHisValValLeuValAsp 160
 SerGlnGluAsnGlyValArgLeuValHisAlaLeuLeuAlaCysAlaGluAlaValGln 180
 LysGluAsnLeuThrValAlaGluAlaLeuValLysGlnIleGlyPheLeuAlaValSer 200
 GlnIleGlyAlaMetArgLysValAlaThrTyrPheAlaGluAlaLeuAlaArgArgIle 220
 TyrArgLeuSerProSerGlnSerProIleAspHisSerLeuSerAspThrLeuGlnMet 240
 HisPheTyrGluThrCysProTyrLeuLysPheAlaHisPheThrAlaAsnGlnAlaIle 260
 LeuGluAlaPheGlnGlyLysLysArgValHisValIleAspPheSerMetSerGlnGly 280
 LeuGlnTrpProAlaLeuMetGlnAlaLeuAlaLeuArgProGlyGlyProProValPhe 300
 ArgLeuThrGlyIleGlyProProAlaProAspAsnPheAspTyrLeuHisGluValGly 320
 CysLysLeuAlaHisLeuAlaGluAlaIleHisValGluPheGluTyrArgGlyPheVal 340
 AlaAsnThrLeuAlaAspLeuAspAlaSerMetLeuGluLeuArgProSerGluIleGlu 360
 SerValAlaValAsnSerValPheGluLeuHisLysLeuLeuGlyArgProGlyAlaIle 380
 AspLysValLeuGlyValValAsnGlnIleLysProGluIlePheThrValValGluGln 400
 GluSerAsnHisAsnSerProIlePheLeuAspArgPheThrGluSerLeuHisTyrTyr 420
 SerThrLeuPheAspSerLeuGluGlyValProSerGlyGlnAspLysValMetSerGlu 440
 ValTyrLeuGlyLysGlnIleCysAsnValValAlaCysAspGlyProAspArgValGlu 460
 ArgHisGluThrLeuSerGlnTrpArgAsnArgPheGlySerAlaGlyPheAlaAlaAla 480
 HisIleGlySerAsnAlaPheLysGlnAlaSerMetLeuLeuAlaLeuPheAsnGlyGly 500
 GluGlyTyrArgValGluGluSerAspGlyCysLeuMetLeuGlyTrpHisThrArgPro 520
 LeuIleAlaThrSerAlaTrpLysLeuSerThrAsn 532

Fig. 4

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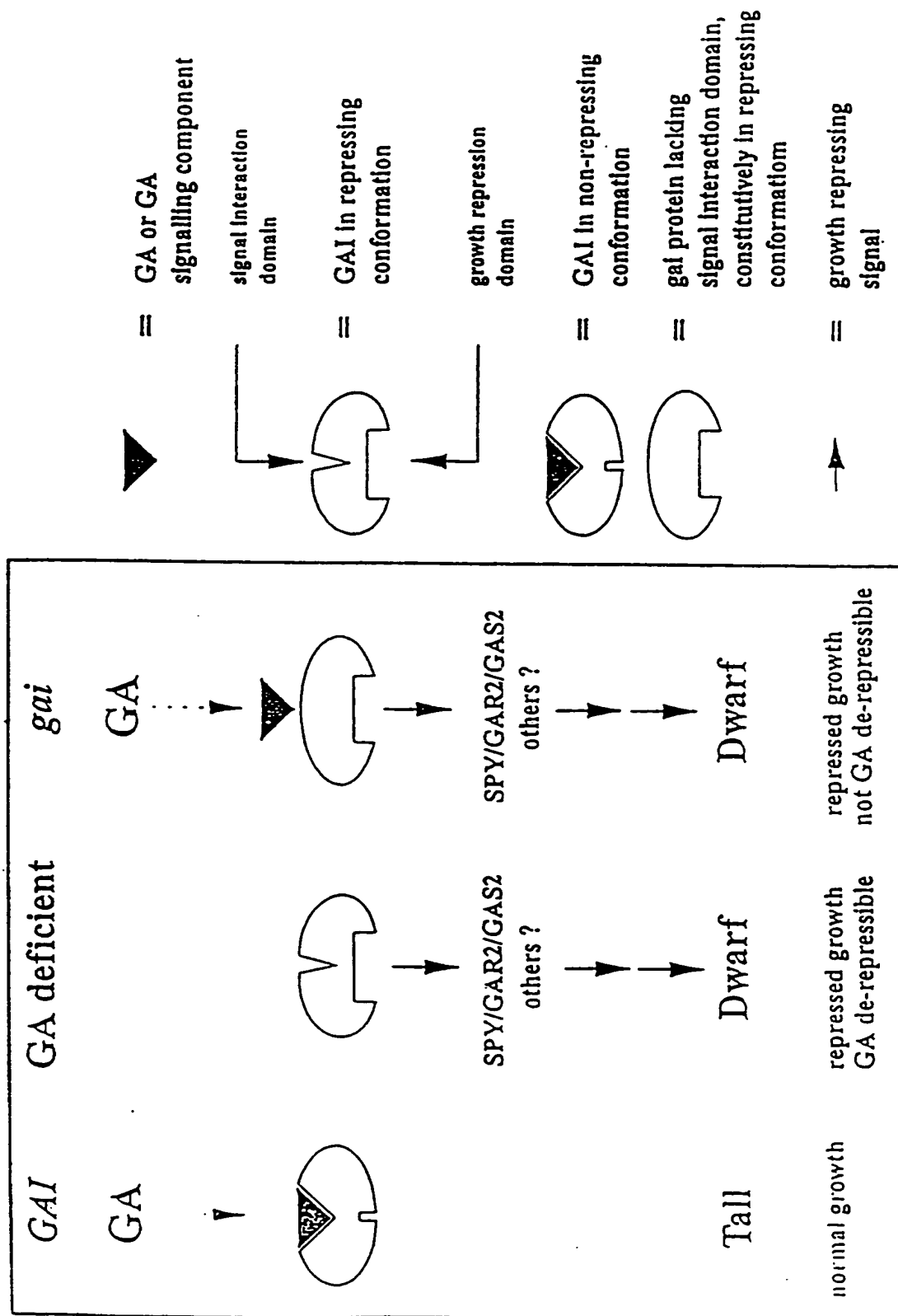


FIG. 5

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Figure 6(a)

1 TAGAAGTGGT AGTCGAGTGA AAAAACAAT CCTAAGCAGT CCTAACCGAT
51 CCCCCAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACCTCGAGC
251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
301 GCTACTGAGA CTGTTCACTA TAATCCGCCG GAGCTTTACA CGTGGCTTGA
351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
401 TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCCG TATCGATTCCG
451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
551 AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGTGTGCGT
601 CTCGTTACAG CGCTTTTGGC TTGCGCTGAA GCTGTTTACA AGGAGAATCT
651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTTCTC
701 AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
751 CGCGCGATTT ACCGTCTCTC TCCGTCGCAG AGTCCAATCG ACCACTCTCT
801 CTCCGATACT CTTTAGATGC ACTTCTACGA GACTTGTCTT TATCTCAAGT
851 TCGCTCACTT CACGGCGAAT CAAGCGATTC TCGAAGCTTT TCAAGGGAAG
901 AAAAGAGTTC ATGTCAATGA TTTCTCTATG AGTCAAGGTC TTCAATGGCC
951 GGCGCTTATG CAGGCTCTTG CGCTTCGACC TGGTGGTCTT CCTGTTTTC
1001 GGTAAACCGG AATTGGTCCA CCGGCACCGG ATAATTTTCA TTATCTTCAT
1051 GAAGTTGGGT GTAAGCTGGC TCATTTAGCT GAGGCGATTC ACGTTGAGTT
1101 TGAGTACAGA GGATTTGTGG CTAACACTTT AGCTGATCTT GATGCTTCCA
1151 TGCTTGAGCT TAGACCAAGT GAGATTGAAT CTGTTGCGGT TAACTCTGTT
1201 TTCGAGCTTC ACAAGCTCTT GGGACGACCT GGTGCGATCG ATAAGGTTCT
1251 TGGTGTGGTG AATCAGATTA AACCAGAGAT TTCACTCTG GTTGAGCAGG
1301 AATCGAACCA TAATAGTCCG ATTTTCTTAG ATCGGTTTAC TGAGTCGTTG
1351 CATTATTACT CGACGTTGTT TGACTCGTTG GAAGGTGTAC CGAGTGGTCA
1401 AGACAAGGTC ATGTCGGAGG TTTACTTGGG TAAACAGATC TGCAACGTTG
1451 TGGCTTGTTA TGGACCTGAC CGAGTTGAGC GTCATGAAAC GTTGAGTCAG
1501 TGGAGGAACC GGTTCGGGTC TGCTGGGTTT GCGGCTGCAC ATATTGCTTC
1551 GAATGCCGTTT AAGCAAGCGA GTATGCTTTT GGCTCTGTTC AACGGCGGTG
1601 AGGGTTATCG GGTGGAGGAG AGTGACGGCT GTCTCATGTT GCG

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Figure 6(b)

1 MKRDHRRHHQ DKRTMMNNEE DDGNGMDVAQ KLEQLVEMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTTNRRLK CSNGVVETTT ATAESTRHVV LVDSQENGVR
151 LVHALLACAE AVQKENLTVA EALVRQIGFL AVSQIGAMRK VATYFAEALA
201 RRIYRLSPSQ SPIDHSLSDT L*

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Figure 6(c)

1 TAGAAGTGGT AGTGGACTCA AAAAACAAT CCTAAGCAGT CCTAACCGAT
 51 CCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
 101 CGACATTGAA GGAAAAACCT TMTAGATCCA TCTCTGAAAA AAAACCAACC
 151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
 201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACCTCGAGC
 251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
 301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
 351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
 401 TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCCG TATCGATTCC
 451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
 501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
 551 AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CCGTGTGCGT
 601 CTCGTTACCG CGCTTTTGGC TTGCGCTGAA GCTGTTTACA AGGAGAACTC
 651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTTCTC
 701 AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
 751 CGGCGGATTT ACCGTCTCTC TCCGTCCGAG AGTCCAATCG ACCACTCTCT
 801 CTCCGATACT CTTGAGATGC ACTTCTACGA GACTTGTCTT TATCTCAAGT
 851 TCGCTCACTT CACGGCGAAT CAAGCGATTG TCGAAGCTTT TCAAGGGAAG
 901 AAAAGAGTTC ATGTCATTGA TTCTCTATGA GTCAAGGTCT TCAATGGCCG
 951 GCGCTTATGC AGGCTCTTGC GCTTCGACCT GGTGGTCCCT CTGTTTCCG
 1001 GTTAACCGGA ATTGGTCCAC CGGCACCGGA TAATTTGAT TATCTTCATG
 1051 AAGTTGGGTG TAAGCTGGCT CATTTAGCTG AGGCGATTCA CGTTGAGTTT
 1101 GAGTACAGAG GATTTGTGGC TAACACTTTA GCTGATCTTG ATGCTTCGAT
 1151 GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTTGCGGTT AACTCTGTTT
 1201 TCGAGCTTCA CAAGCTCTTG GGACGACCTG GTGCGATCGA TAAGGTCTTT
 1251 GGTGTGGTGA ATCAGATTAA ACCGGAGATT TCACTGTGG TTGAGCAGGA
 1301 ATCGAACCAT AATAGTCCGA TTTTCTTAGA TCGGTTTACT GAGTCGTTGC
 1351 ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC GACTGGTCAA
 1401 GACAAGGTCA TGTCGGAGGT TTAATTGGGT AAACAGATCT GCAACGTTGT
 1451 GGCTTGTGAT GGACCTGACC GAGTTGAGCG TCATGAAACG TTGAGTCACT
 1501 GGACGAACCG GTTCGGGTCT GCTGGGTTTG CGGCTGCACA TATTGGTTCTG
 1551 AATGCGTTTA AGCAAGCGAG TATGCTTTTG GCTCTGTTCA ACGGCGGTGA
 1601 GGGTTATCGG GTGGAGGAGA GTGACGGCTC TCTCATCTTG GG

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Figure 6(d)

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1  MKRDEHHHHHQ DKRTMMNNEE DDGNGMDVAQ KLEQLEVMMS NVQEDDLSQL
51  ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTINKRLK CSNGVVETTT ATAESTRHVV LVDSQENGVR
151 LVHALLACAE AVQKENLTV AALVKQIGFL AVSQIGAMRK VATYFAEALA
201 RRIYRLSPSQ SPIDHSLSDT LQMHFYETCP YLKFAHFTAN QAILEAFQ GK
251 KRVHVIDSL*

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Figure 6(e)

1 TAGAAGTGGT AGTGGAGTGA AAAAACAAT CCTAAGCAGT CCTAACCGAT
51 CCCCCAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACCTCGAGC
251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
401 TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCGC TATCGATTCCG
451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
551 AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGTGTGCGT
601 CTCGTTACAG CGCTTTTGGC TTGCGCTGAA GCTGTTCAGA AGGAGAATCT
651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTTCTC
701 AAATCGGAGC TATGAGAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
751 CGGCGGATTT ACCGTCTCTC TCCGTGCGAG AGTCCAATCG ACCACTCTCT
801 CTCCGATACT CTTCAGATGC ACTTCTACGA GACTTGTCCT TATCTCAAGT
851 TCGCTCACTT CACGGCGAAT CAAGCGATTC TCGAAGCTTT TCAAGGGAAG
901 AAAAGAGTTC ATGTCATTGA TTTCTCTATG AGTCAAGGTC TTGGGCGCTT
951 ATGCAGGCTC TTGCGCTTCG ACCTGGTGGT CCTCCTGTTT TCCGGTTAAC
1001 CGGAATTGGT CCACCGGCAC CGGATAATTT CGATTATCTT CATGAAGTTG
1051 GGTGTAAGCT GGCTCATTTA GCTGAGGCGA TTCACGTTGA GTTTGAGTAC
1101 AGAGGATTTG TGGCTAACAC TTTAGCTGAT CTTGATGCTT CGATGCTTGA
1151 GCTTAGACCA AGTGAGATTG AATCTGTTGC GGTAACTCT GTTTTCGAGC
1201 TTCACAAGCT CTTGGGACGA CCTGGTGCGA TCGATAAGGT TCTTGGTGTG
1251 GTGAATCAGA TTAAACCGGA GATTTTCACT GTGGTTGAGC AGGAATCGAA
1301 CCATAATAGT CCGATTTTCT TAGATCGGTT TACTGAGTCG TTGCATTATT
1351 ACTCGACGTT GTTTGACTCG TTGGAAGGTG TACCGAGTGG TCAAGACAAG
1401 GTCATGTCGG AGGTTTACTT GGGTAAACAG ATCTGCAACG TTGTGGCTTG
1451 TGATGGACCT GACCGAGTTG AGCGTCATGA AACGTTGAGT CAGTGGAGGA
1501 ACCGGTTCGG GTCTGCTGGG TTTGCGGCTG CACATATTGG TTCCAATCGG
1551 TTAAAGCAAG CGAGTATGCT TTTGGCTCTG TTCAACGGCG GTGAGGGTTA
1601 TCGCGTGGAG GACAGTGACG GCTGTCTCAT GTTGGG

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Figure 6(f)

1 MKRDHHHHHQ DKKTMMNNEE DDGNGMDVAQ KLEQLEVMMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTTNKRLK CSNGVVETTT ATAESTREVV LVDSQENGVR
151 LVHALLACAE AVQKENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA
201 RRIYRLSPSQ SPIDHSLSDT LQMEFYETCP YLXFAHFTAN QAILEAFQGX
251 KRVHVIDFSM SQGLGRLCRL LRFDLVVLLF SG*

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Figure 6(g)

1 TAGAAGTGGT AGTGGAGTGA AAAAACAAT CCTAAGCAGT CCTAACCGAT
 51 CCCCAGAGCT AAAGATTCTT CACCTTCCCA AATAAGCAA AACCTAGATC
 101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
 151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
 201 GAATGAAGAA GACGACGGA ACGGCATGGA TGTGCTCAG AAACCTGAGC
 251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
 301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
 351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
 401 TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCCG TATCGATTCC
 451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
 501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
 551 AGTCAACTCG GCATGTGTCC TGGTTGACTC GCAGGAGAAC GGTGTGCGTC
 601 TCGTTCACGC GCTTTTGGCT TCGCTGAAG CTGTTGAGAA GGAGAATCTG
 651 ACTGTGGCGG AAGCTCTGGT GAAGCAAATC GGATTCTTAG CTGTTTCTCA
 701 AATCGGAGCT ATGAGAAAAG TCGCTACTTA CTTGCGCGAA GCTCTCGCGC
 751 GCGGATTFTA CCGTCTCTCT CCGTCGAGA GTCCAATCGA CCACTCTCTC
 801 TCCGATACTC TTCAGATGCA CTTCTACGAG ACTTGTCTTT ATCTCAAGTT
 851 CGCTCACTTC ACCGCGAATC AAGCGATTCT CGAAGCTTTT CAAGGGAAGA
 901 AAAGAGTTCA TGTCATTGAT TTCTCTATGA GTCAAGGTCT TCAATGGCCG
 951 GCGCTTATGC AGGCTCTTGC GCTTCGACCT GGTGGTCCTC CTGTTTTCCG
 1001 GTTAACCGGA ATTGGTCCAC CGGCACCGGA TAATTTGAT TATCTTCATG
 1051 AAGTTGGGTG TAAGCTGGCT CATTTAGCTG AGGCGATTCA CGTTGAGTTT
 1101 GAGTACAGAG GATTGTGGC TAACACTTTA GCTGATCTTG ATGCTTCGAT
 1151 GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTGCGGTT AACTCTGTTT
 1201 TCGAGCTTCA CAAGCTCTTG GGACGACCTG GTGCGATCGA TAAGGTTCTT
 1251 GGTGTGGTGA ATCAGATTAA ACCGGAGATT TTCCTCTGG TTGAGCAGGA
 1301 ATCGAACCAT AATAGTCCGA TTTTCTTAGA TCGGTTTACT GAGTCGTTGC
 1351 ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC GAGTGGTCAA
 1401 GACAAGGTCA TGTCGGAGGT TACTTGGGT AAACAGATCT GCAACGTTGT
 1451 GGCTTGTGAT GGACCTGACC GAGTTGAGCG TCATGAAACG TTGAGTCAGT
 1501 GGAGGAACCG GTTCGGGTCT GCTGGGTTTG CGGCTGCACA TATTGGTTCC
 1551 AATGCGTTTA AGCAAGCGAG TATGCTTTTG GCTCTGTTCA ACGGCGGTGA
 1601 GCGTTATCGG GTGGAGGAGA GTGACGGCTG TCTCATGTTG GG

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Figure 6(h)

1 MKRDHHEHHQ DKKTMNNNEE DDGNGHDVAQ KLEQLEVMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTTNKRLK CSNGVVEITT ATAESTRHVS WLTRRRITCV
151 SFTRFWLALK LFRRI*

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